

ResMultNet-50: An automatic medical Image Diagnosis approach for lung diseases using deep transfer learning

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Abstract—Lung diseases such as Covid-19, Pneumonia and Tuberculosis remains to be among the leading causes of deaths globally. These diseases present themselves in a similar manner bearing common signs and symptoms such as coughing, fever, fatigue and shortness of breaths. To prevent adverse effects of these diseases and save more lives, early detection and diagnosis of the aforementioned diseases is necessary. This paper proposes a deep transfer learning model: ResMultNet-50 to assist radiologists in their work while adopting inverse class weighting approach to handle class imbalance problem. The proposed approach relied on fine-tuned ResNet-50 for the diagnostic task of detecting the three respiratory diseases from chest x-rays. In the study, a data set comprising of 13,188 chest x-ray images was used and the proposed approach achieved an average accuracy of 96.12%. This model outperformed other deep learning models and transfer learning models used in the previous studies for solving multi-class related problems.

Index Terms—Transfer learning, deep learning, ResNet-50, Covid-19, Pneumonia, Tuberculosis

I. INTRODUCTION

Lung related diseases are among the leading causes of deaths across the globe affecting all categories of people ranging from children to adults. Some of these diseases include Pneumonia, Covid-19, and Tuberculosis [1]. Pneumonia is a respiratory disease that affects the lungs, and is caused by either Virus, Bacteria or Fungi. According to World Health Organization (WHO) reports, the disease claimed over 740,180 children in 2019 which accounted for 14% of deaths in children below 5 years [2]. Covid-19 is another respiratory disease that affects the lungs, and is caused by SARS-COV-2 virus [3]. The disease was first discovered in Wuhan, China in 2019 [4]. Since then, it has spread all over the world claiming over 6.9 million people, and over 767 million have been affected [5]. Another disease affecting people is Tuberculosis which is caused by Mycobacterium, that majorly affects the lungs [6]. In 2021, the disease was reported to claim 1.6 million people with over 10.6 million people affected the same year [7]. The most common signs and symptoms for these three diseases involves coughing, fever, shortness of breath and fatigue. Due to their rampant spread, these diseases require early

diagnosis and treatment to ensure they are timely managed and reduce the stress in the healthcare systems [9].

Polymerase Chain Reaction (PCR) assays, which are the gold standard method for detecting Covid-19, are the most often used methodology due to its high sensitivity and specificity. Antigen and Antibody testing are two alternative methods for identifying the illness [10]. The Mantoux skin test is used to diagnose tuberculosis, whereas blood and sputum tests are used to diagnose pneumonia [11]. Despite the fact that these treatments are popular and gold standards for treating various disorders owing to their specialized nature, they are time consuming, laborious, and manual [12]. At the same time, these tests are sometimes characterized to producing high false positives leading to wrong treatment and medication [13].

Other alternative ways to detecting Covid-19, Pneumonia and Tuberculosis is through use of radiography examination, where different medical imaging modalities such as Chest x-rays (CXR), Computed Tomography (CT) scans and Magnetic Resonance Imaging (MRI) are used. These modalities presents different visual indicators associated with each of the diseases mentioned, and requires experts for interpretation. For instance, Covid-19 presents itself with signs of Ground Glass Opacities (GGO) [14], Pneumonia shows fluid and inflammation buildup in the lungs [15] while Tuberculosis shows patchy infiltrates, nodules or fibrosis [16]. CXR imaging is the most widely used initial modality for examining the presence of the disease in a patient [17]. The modality is cheap, and exposes the patients to low ionizing radiation in comparison to the others [18]. However, the modality necessitates the need of professionals (radiologists) for analysis in order to properly identify a patient and treat them. These professionals, however, are few, particularly in middle-income nations [19] and to save more more lives, technology related approaches need to be adopted to assist radiologists in their work, and at the same time, promote automation in healthcare industries.

Deep transfer learning, an approach in deep learning (machine learning) paradigms, is one of those technology

based methods that can aid in the diagnosis of respiratory disorders like Covid-19, Pneumonia and Tuberculosis. It involves the transfer of knowledge from one domain to another but related domain [20]. The technology is characterized by use of small datasets, a feature that is evidenced in the healthcare industries where getting large amounts of data for automation is a huge problem. In recent days, deep transfer learning has been used to detect different respiratory diseases like Covid-19 [21], Pneumonia [22] and Tuberculosis [23]. Despite the good performances it has shown, it has been realised that the approach suffers from class imbalance problems, brought about by the variations in the number of samples for the diseases. In layman's understanding, given two diseases: Pneumonia and Covid-19, the class imbalance problem occurs when while training a deep transfer learning model for automation, the size of data for Pneumonia is so much larger than that of Covid-19 meaning that the trained model predicts in favor of the majority class. To tackle this problem, this research proposes a technique that leverages deep transfer learning to provide an accurate, real-time and faster automation method for detection of Covid-19, Pneumonia and Tuberculosis from chest x-ray images.

ResNet-50 is a pre-trained deep CNN network that is 50 layers deep. It employs skip connections to overcome the vanishing gradient in CNN networks, where the original inputs are added to the output of the network's convolution blocks [34]. In the medical image detection tasks, the network has been achieving state of the art performances making it an ideal choice for our proposed work. In the ILSVRC 2015 image classification competition, the model won the first place in the competition with 0.75 top - 1 accuracy [36].

The rest of this paper is organized with Literature review work in Sect. II, Proposed approach in Sect. III, Results in Sect. IV, Discussion and Conclusion in Sect. V.

II. LITERATURE REVIEW

Detection of lung diseases such as Covid-19, Pneumonia and Tuberculosis requires exploration of different techniques for timely detection, treatment and containment of these infections, especially in the context of global health crisis. However, this task is highly limited due to factors like class imbalance problems, limited datasets and need for high performances with reduced bias. To solve these problems, different techniques are considered.

A. Transfer Learning Approaches

Different machine learning techniques, in the category of deep transfer learning have been widely looked upon. These include the use of Conventional Transfer Learning (CTL), Domain Adaptation Transfer Learning and Multi-Task Transfer Learning (MTL).

With CTL, pre-trained models are used as feature extractors in the input and pooling layers of deep learning architectures, while utilizing the traditional machine learning techniques like Support Vector Machines (SVM), Random

Forest (RF), and Naive Bayes (NB) in the fully connected layers as classifiers [24]. On the other hand, MTL is a deep transfer learning approach that involves use of a single model to perform multiple related tasks simultaneously. The model learns a shared set of feature representations that can be used to perform each task, as well as task-specific layers that allow it to specialize for each task. By doing so, multi-task transfer learning allows the model to leverage the shared knowledge across tasks and learn more robust and generalize features [25]. In Domain adaptation TL, the goal is always to learn features that are robust to the domain shift which is the differences between the source domain, D_S (where the model is trained) and the target domain, D_T (where the model is applied). Based on the domain classes, TL is classified as homogeneous or heterogeneous. The categories vary based of feature spaces and label spaces between D_S and D_T . With homogeneous TL, $X_S = X_T$ and $Y_S = Y_T$ while in heterogeneous TL,

$$X_S \neq X_T \quad (1)$$

$$Y_S \neq Y_T \quad (2)$$

where X represents the feature spaces and Y represent the label spaces [26]. The approach of domain TL is achieved through fine tuning the pre-trained model on a small amount of labelled data from D_T , while keeping the weights of the lower layers fixed and by doing so, the model is able to learn without over-fitting to the limited labelled data.

Several works has been done in the recent times using either of the deep transfer learning approach described. For instance, Multi-task TL was used in the experimental works of [27] to aid diagnose Covid-19, Pneumonia, and Tuberculosis in chest X-rays. The data set used had a total of 6386 images constituting Covid-19, Pneumonia, Tuberculosis and healthy images. These images were pre-processed by reducing noise, normalizing the images and applying different augmentation techniques such as rotation, width shift range, height shift range and ZCA whitening. The dataset was split into 70% and 30% using Monte Carlo cross-validation split and Categorical cross-entropy method was used as a cost function. The authors optimized their training by use of SGD loss function, 0.001 learning rate and 30 epochs. These were applied to DenseNet-121 and ResNet-50 pre-trained models with average recall of 62.7% and 62.0% respectively. This study however utilized very few images of the diseases which were imbalanced with 209 Covid-19 images, 4341 Pneumonia images and 468 Tuberculosis images.

[29] adopted a multi-task transfer learning approach for the detection of Pneumonia, Tuberculosis and Normal instances using a data set of 1071 (388 normal, 500 Pneumonia, 303 TB) chest X-ray images obtained from Clinical labs of Mumbai, India. The data set was pre-processed through resizing (64x64), and normalization [0-255] before being split into 80%20% ratio for training and testing respectively. In the training, the researchers used VGG-16 classifier with

Adam optimizer and 0.001 learning rate. From the 12 epochs used, the resulting accuracy of their model was 98%. However, the research work was limited due to use of very small data set which cannot be used to generalize the real world situation with so many people. At the same time, the data set used was imbalanced in some way with few samples of TB compared to other instances. As a result of these limitations, there was a high possibility of model over-fitting with majority class being favored.

B. Class imbalance

The distribution of different disease instances have been a huge problem in ensuring each disease class is treated equally, due to huge disparities in the number of instances. Researchers have adopted methods like sampling techniques, change of class weight methods and augmentation techniques.

Manipulation of the dataset is used in sampling procedures to achieve a more balanced distribution of classes. Oversampling is the practice of raising the number of minority class samples while decreasing the number of majority class samples. To balance the classes, synthetic sampling methods such as SMOTE (Synthetic Minority Over-sampling Technique) produce synthetic samples. The fundamental objective for employing sampling methods is to alleviate the issue of class imbalance. Machine learning algorithms may learn more successfully from both ill and normal instances if a more balanced dataset is created. This leads to enhanced generalization and performance, particularly in the face of skewed input. Despite the pros of the approach, more generated artificial images resulted to more computational resources for training of the models and possible over-fitting of the model [30].

During model training, class weights change each class's contribution to the loss function. By giving additional weight to minority groups, the model is punished for misclassifying these situations. This encourages the model to pay more attention to minority groups, lowering the possibility of false negatives. Changing class weights addresses class imbalance without changing the dataset itself. It directs the model to concentrate on minority groups, ensuring that illnesses such as COVID-19, pneumonia, and TB are not missed [31]. It is a computationally efficient method that does not need data processing.

Data augmentation is the process of producing additional training samples from existing data by performing different transformations (e.g., rotation, scaling, and flipping). This broadens the training dataset's variety without requiring new data collecting. When working with little datasets, data augmentation comes in handy. The effective dataset size is enhanced by creating augmented samples, lowering the danger of overfitting. Augmentation also improves model resilience by exposing it to a broader variety of variability seen in real-world data. Such techniques was employed in the successful work of image classification using deep learning techniques [32].

III. PROPOSED METHODOLOGY

The proposed approach followed four major steps: Creating an amalgam of suitable dataset, pre-processing the dataset, building a model architecture based on ResNet50 and finally, training and evaluating our model. The followed process is depicted in Fig. 1.

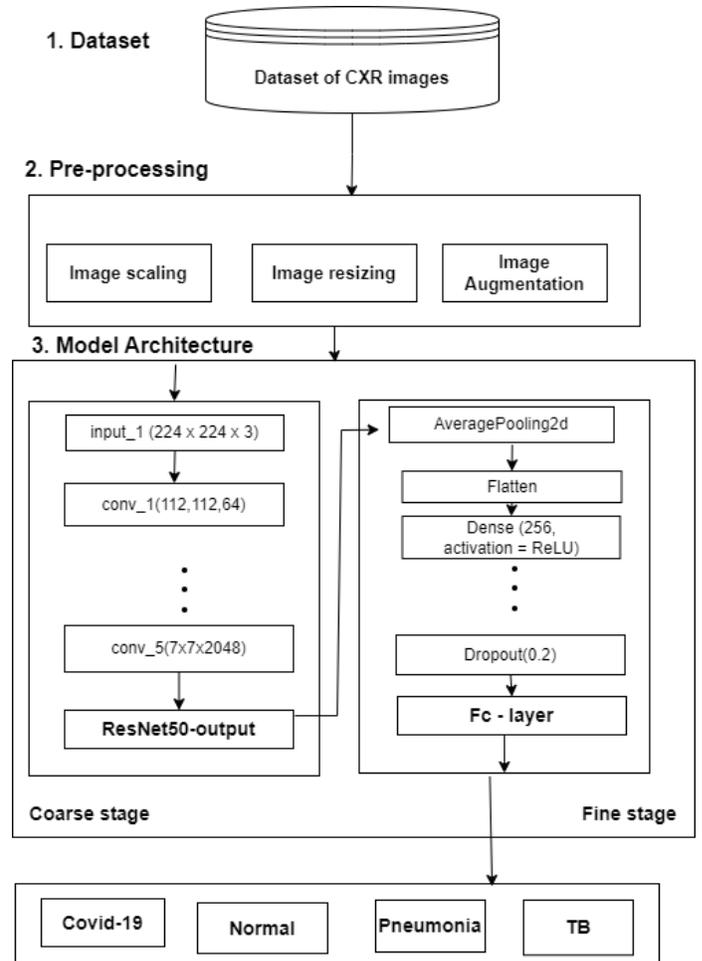


Fig. 1. Proposed methodological approach

A. Dataset

Finding a suitable dataset in a single repository containing Covid-19, Pneumonia, Tuberculosis and Normal cases for healthy patients is very difficult. This work involved creating an amalgam of verified and tested dataset obtained from different publicly available dataset sources like Kaggle. These dataset had been screened for quality and correct labelling by different radiologists and medical practitioners. We were able to have a dataset consisting of 3616 Covid-19 cases, 4599 Normal instances [33] [34], 4273 Pneumonia cases [35], and 700 Tuberculosis cases was used [36]. For Pneumonia, a combination of viral and bacterial pneumonia cases was combined bearing different resolutions. The chest x-ray images for the whole dataset were of different

resolutions, sizes and formats. At the same time, the datasets images were gray scale in nature, and to obtain the fine details of them, further pre-processing was required.

B. Pre-processing

The CXR images were pre-processed in two phases: (1) Image resizing, and (2) Image augmentation.

- Phase 1: Image resizing Due to the differences in the resolutions of the images in the dataset, all images were resized to a common size of 224×224 pixels.
- Phase 2: Image augmentation To increase the quality of the resized images and number of images for the training of the model, data augmentation technique was used. Data augmentation creates new instances of images by altering slightly the pixel values of the images, which helps to prevent over fitting of the model. Image augmentation techniques used in our research involved changing the brightness of the images (by a factor between 0.67 and 1.33) and changing the contrast by the same factor.

C. Model Architecture

Our proposed ResMultNet-50 architecture comprised of two broad stages described as (1) course stage and (2) fine stage predictions.

In the coarse-stage predictions, the model used was a pre-trained ResNet-50 to extract features from the input CXR images. As a fixed feature extractor, the model required freezing of several layers. Through trial and error approach, the best feature extracting criteria allowed us to freeze 10 lower layers of the original ResNet-50. The features obtained in this step were subsequently processed through a series of fully connected layers to give an approximate coarse forecast of the diseases. The output of the coarse-stage classification was a probability vector of size 4, corresponding to the four classes of interest: COVID-19, pneumonia, tuberculosis, and Normal instances. This output was fed to next stage of processing, which was fine stage.

In the fine-stage classification, the model used was a customized CNN to refine the coarse prediction generated in the first stage. Specifically, the CNN is trained to identify and extract more specific features from the input image, which are then pooled together with the help of pooling layers. To reduce over fitting of the model, two dropout layers were used. The output of the fine-stage classification was the final probability vector of size 4, which represented the refined predictions of the diseases.

D. Training and Evaluation

ResMultNet-50 model required setting the initial parameters for the training of the model. The parameters included a learning rate of 0.001, 15 epochs, loss function of sparse categorical cross entropy and a batch size of 32. For the fully classification layer of our model, softmax activation function was used. To minimize the effects of class imbalance, 40

we incorporated class weighting approach method in our categorical loss function.

Our model was evaluated based on recall, precision, accuracy and F1-score. These metrics are widely used especially in the prediction of multiclass related problems which relies of four factors: True positive (TP) which is the number of positive samples that are correctly classified as positive, true negative (TN) which is the number of negative samples that are correctly classified as negative, false positive (FP) which is the number of negative samples that are incorrectly classified as positive, and false negative (FN) which is the number of positive samples that are incorrectly classified as negative. Based on the highlighted factors; recall, precision, accuracy and F1-score of our model was obtained.

Recall is the percentage of correctly classified CXR images out of all classified images.

$$Recall = \frac{TP}{TP + FN} \quad (3)$$

Precision is the percentage of correctly classified CXR images in relation to the total number of classified images.

$$Precision = \frac{TP}{TP + FP} \quad (4)$$

Accuracy is the total number of correct predictions made, divided by the total number of all predictions.

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \quad (5)$$

F1-Score combines precision and recall. It measures how good the model is. Given by the formula

$$F1 - Score = \frac{2 * (precision * recall)}{precision + recall} \quad (6)$$

IV. RESULTS

A. Dataset exploratory analysis

The experimental analysis of our approach involved doing the exploratory analysis of our data first before pre-processing, building and training of the model. The distribution of data showed that Normal instances were more, followed by Pneumonia cases with Tuberculosis instances being the least.

In terms of percentages, Pneumonia cases accounted for 32%, Normal instances of healthy patients accounted for 35% of the whole dataset, Covid-19 for 27% while Tuberculosis instances accounted for 5%. This was the main drawback with this dataset and to provide reliable results without bias, class weighting, transfer learning and data augmentation methods were used, as opposed to application of sampling techniques.

B. Class Weighting approach to handling class imbalance

Given our multi-class problem of detecting different respiratory diseases, our classes were very imbalanced. If the

samples were used in this way, our predictions would favor the majority class which is Normal instances for healthy patients. To avoid this problem, we proposed an inverse class weighting approach based on the frequency of each class in the training set. The approach was based on loss function chosen which was categorical cross entropy loss, defined as

$$\mathcal{L}_{cross-entropy} = -\frac{1}{N} \sum_{i=1}^N [y_i \log(\hat{y}_i) + (1 - y_i) \log(1 - \hat{y}_i)] \quad (7)$$

where, \hat{y} is the predicted class, and y is the actual class y_i is the i^{th} sample of y and \hat{y}_i is the i^{th} sample of \hat{y} and N is the total number of training samples.

Using the loss function, we created a bias towards the majority class, which was achieved by creating multipliers or weights to balance the loss function. We ended up with a modified loss function

$$\mathcal{L}_{cross-entropy} = -\frac{1}{N} \sum_{i=1}^N [w_p y_i \log(\hat{y}_i) + w_n (1 - y_i) \log(1 - \hat{y}_i)] \quad (8)$$

With the new loss function, our role was to compute w_p and w_n , which were obtained as proportions for each class in the training set. For w_p (weight for the majority class):

$$w_p = \frac{N}{4 \cdot N_p} \quad (9)$$

For w_n (weight for the minority classes):

$$w_n = \frac{N}{4 \cdot \sum_{i=1}^3 N_i} \quad (10)$$

where N_p denotes the number of samples in the majority class, N_i represents the number of samples in each of the three minority classes and 4 represents the number of classes in our training set: Normal, Covid-19, Pneumonia and Tuberculosis. The obtained weights are passed to the model during training.

C. Experimental results

Our proposed ResMultNet-50 was aimed at automating the process of diagnosis and assisting radiologists in their work of examining chest radiography for the detection of Covid-19, Pneumonia and Tuberculosis. After training our model for 15 epochs, an average accuracy of 0.9612 was obtained. The other metrics used were precision, recall and F1-score. The overall results of our model were impressive as shown in Table I below. The training and validation accuracies of our model was seen to have an upward trend.

On the other hand, their respecting training and validation losses were observed to be on a downward trend. The accuracy and loss trends of our ResMultNet-50 showed that our model learned well to the data we provided. After these analysis, we went ahead and tried to do predictions of our model and check whether it was good for use. To our

TABLE I
EXPERIMENTAL RESULTS

Class	Precision	Recall	F1-Score
Covid-19	0.9426	0.9600	0.9512
Normal	0.9488	0.9396	0.9442
Pneumonia	0.9843	0.9792	0.9818
Tuberculosis	1.0000	1.0000	1.0000

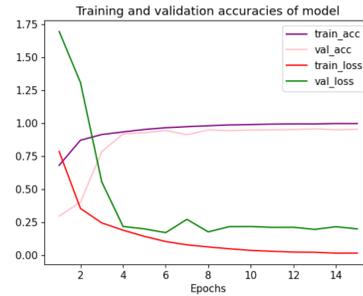


Fig. 2. Accuracy and Loss performances

expectations of our model, it was able to accurately predict each disease to its respective class labels.

V. DISCUSSION AND CONCLUSION

Transfer learning approaches, use of data augmentation and inverse class weighting approach produces best results for detection of Covid-19, Pneumonia and Tuberculosis. As found in this research, our ResMultNet50 model can help the few radiologists in the industry diagnose the aforementioned illness with high degree of accuracy.

Comparing this model with other state of the art models, as given Table II, our model showed improved performances, which was a huge contribution in the work.

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TABLE II
COMPARATIVE ANALYSIS

Cases	Method	Accuracy	Author
Normal = 1583 Covid-19 = 576 Pneumonia = 4273 Tuberculosis = 700	Custom CNN	0.9594	[39]
Normal = 439 Covid-19 = 435 Bacterial Pneumonia = 439 Viral Pneumonia = 439 Tuberculosis = 434	Transfer learning of ResNet-50 with Ensemble of discriminant classifier	0.9160	[40]
Normal = 1583 Covid-19 = 576 Pneumonia = 4273 Tuberculosis = 155	Custom CNN	0.9120	[41]
Normal = 4599 Covid-19 = 3616 Pneumonia = 4273 Tuberculosis = 700	Fine tuned ResNet-50	0.9612	Ours

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